

SEQUENCE LISTING

<110> Sheppard, Paul O.
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 Haldeman, Betty A.
 Grant, Francis J.

<120> INTERFERON-LIKE PROTEIN ZCYTO21

<130> 01-18

<150> 60/285,424

<151> 2001-04-20

<150> 60/215,446

<151> 2000-06-30

<160> 16

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(603)

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gcc gtg gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag	96
Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys	
20 25 30	
ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg	144
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala	
35 40 45	
agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa	192
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys	
50 55 60	
aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg	240
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg	
65 70 75 80	
ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc	288
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala	
85 90 95	
ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac	336
Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp	
100 105 110	
gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc	384

Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu		
		115					120					125					
cag	gcc	tgt	atc	cag	cct	cag	ccc	aca	gca	ggg	ccc	agg	ccc	cgg	ggc		432
Gln	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly		
	130					135				140							
cgc	ctc	cac	cac	tgg	ctg	cac	cgg	ctc	cag	gag	gcc	ccc	aaa	aag	gag		480
Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu		
145				150				155							160		
tcc	gct	ggc	tgc	ctg	gag	gca	tct	gtc	acc	ttc	aac	ctc	ttc	cgc	ctc		528
Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu		
				165				170						175			
ctc	acg	cga	gac	ctc	aaa	tat	gtg	gcc	gat	ggg	gac	ctg	tgt	ctg	aga		576
Leu	Thr	Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Cys	Leu	Arg		
			180					185					190				
acg	tca	acc	cac	cct	gag	tcc	acc	tga									603
Thr	Ser	Thr	His	Pro	Glu	Ser	Thr	*									
		195					200										

<210> 2
 <211> 200
 <212> PRT
 <213> Homo sapiens

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			20					25						30			
Gly	Cys	His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala		
		35					40					45					
Ser	Phe	Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys		
	50					55					60						
Asn	Trp	Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg		
65				70						75				80			
Leu	Leu	Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala		
			85						90					95			
Leu	Thr	Leu	Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp		
			100					105					110				
Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu		
		115					120					125					
Gln	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly		
	130					135					140						
Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu		
145					150					155					160		
Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu		
				165				170						175			
Leu	Thr	Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu	Cys	Leu	Arg		
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Thr	Ser	Thr	His	Pro	Glu	Ser	Thr										
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 <213> Artificial Sequence

<220>
 <223> degenerate sequence

<221> misc_feature
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wsnytnwsnc encargaryt ngcnwsntty aaraargcnm gngaygcnyt ngargarwsn 180
ytnaarytna araaytggws ntgywsnwsn ccngtnttyc cnggnaaytg ggayytnmgn 240
ytnytnrcarg tnmngngarmg nccngtngcn ytnngargcng arytngcnyt nacnytnaar 300
gtnytnrgarg cngcngcngg nccngcnytn gargaygtny tngaycarcc nytnrcayacn 360
ytncaycaya thytnwsnca rytncargcn tgyathcarc cncarccnac ngcnggnccn 420
mgnccnmgng gnmngnytnca ycaytggytn caymgnytn argargcncc naaraargar 480
wsngcnggnt gyytnrgargc nwsngtnacn ttyaayytnt tymgnytnyt nachmngngay 540
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<210> 4
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(603)

<400> 4

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Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
1          5          10          15

gcc gtg gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag      96
Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
          20          25          30

ggc tgc cac att ggc agg ttc aaa tct ctg tea cca cag gag cta gcg      144
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
          35          40          45

agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa      192
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
          50          55          60

aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg      240
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
          65          70          75          80

ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc      288
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
          85          90          95

ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac      336
Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
          100          105          110

gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc      384
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
          115          120          125
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cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc	432
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly	
130 135 140	
cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag	480
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu	
145 150 155 160	
tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc	528
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu	
165 170 175	
ctc acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga	576
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg	
180 185 190	
acg tca acc cac cct gag tcc acc tga	603
Thr Ser Thr His Pro Glu Ser Thr *	
195 200	

<210> 5
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 <212> PRT
 <213> Homo sapiens

<400> 5	
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20 25 30	
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala	
35 40 45	
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys	
50 55 60	
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg	
65 70 75 80	
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala	
85 90 95	
Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp	
100 105 110	
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu	
115 120 125	
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly	
130 135 140	
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu	
145 150 155 160	
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu	
165 170 175	
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg	
180 185 190	
Thr Ser Thr His Pro Glu Ser Thr	
195 200	

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 <213> Homo sapiens

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 <221> CDS
 <222> (98)...(700)

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agagccatgc cgctgggggaa gcagttgcga tttagcc atg gct gca gct tgg acc 115
Met Ala Ala Ala Trp Thr
1 5

gtg gtg ctg gtg act ttg gtg cta ggc ttg gcc gtg gca ggc cct gtc 163
Val Val Leu Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val
10 15 20

ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg 211
Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
25 30 35

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg 259
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
40 45 50

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct 307
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
55 60 65 70

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag 355
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
75 80 85

ggc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg 403
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
90 95 100

gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt 451
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
105 110 115

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 499
His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
120 125 130

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg 547
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
135 140 145 150

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag 595
His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
155 160 165

gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa 643
Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
170 175 180

tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca acc cac cct gag 691
Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu
185 190 195

tcc acc tga caccacacac cttatttatg cgctgagccc tactccttcc 740
Ser Thr *
200

ttaatttatt tcctctcacc ctttatttat gaagctgcag ccctgactga gacatagggc 800
tgagtttatt gttttacttt tatacattat gcacaaataa acaacaagga attgga 856

<210> 7
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 7

Met	Ala	Ala	Ala	Trp	Thr	Val	Val	Leu	Val	Thr	Leu	Val	Leu	Gly	Leu
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Ala	Val	Ala	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys
			20					25						30	
Gly	Cys	His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala
		35					40					45			
Ser	Phe	Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys
		50				55					60				
Asn	Trp	Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg
65					70					75				80	
Leu	Leu	Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala
			85						90					95	
Leu	Thr	Leu	Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp
			100				105						110		
Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu
		115					120					125			
Gln	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly
	130					135					140				
Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu
145					150					155				160	
Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu
			165						170					175	
Leu	Thr	Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asn	Leu	Cys	Leu	Arg
			180				185						190		
Thr	Ser	Thr	His	Pro	Glu	Ser	Thr								
		195					200								

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<220>

<221> CDS

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Gly Ser Ser Cys Asp Leu Ala Met Ala Ala Ala Trp Thr Val Val Leu	
15 20 25	
gtg act ttg gtg cta ggc ttg gcc gtg gca ggc cct gtc ccc act tcc	148
Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val Pro Thr Ser	
30 35 40	
aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa tct	196
Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser	
45 50 55 60	
ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc ttg	244
Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu	
65 70 75	

gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc ttc	292
Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe	
80 85 90	
ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct gtg	340
Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val	
95 100 105	
gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc gct	388
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala	
110 115 120	
gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc ctg	436
Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu	
125 130 135 140	
cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc aca	484
His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr	
145 150 155	
gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg ctc	532
Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu	
160 165 170	
cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct gtc	580
Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val	
175 180 185	
acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg gcc	628
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala	
190 195 200	
gat ggg gac ctg tgt ctg aga acg tca acc cac cct gag tcc acc tga	676
Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr His Pro Glu Ser Thr *	
205 210 215	

<210> 9
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 <212> PRT
 <213> Homo sapiens

<400> 9	
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Leu Gly Leu Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr	
35 40 45	
Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln	
50 55 60	
Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu	
65 70 75 80	
Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp	
85 90 95	
Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala	
100 105 110	
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala	
115 120 125	
Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu	
130 135 140	

Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg
 145 150 155 160
 Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro
 165 170 175
 Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu
 180 185 190
 Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu
 195 200 205
 Cys Leu Arg Thr Ser Thr His Pro Glu Ser Thr
 210 215

<210> 10
 <211> 660
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> degenerate sequence

<221> misc_feature
 <222> (1)...(660)
 <223> n = A,T,C or G

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 gtncnacnw snaarccnac nacnacngn aarggntgyc ayathggnmg nttyaarwsn 180
 ytnwsncnc argarytn gc nwsnttyaar aargcnmgng aygcnytn ga rgarwsnytn 240
 aarytnaara aytggwsntg ywsnwsnccn gtnttyccng gnaaytggga yytnmgnytn 300
 ytn c argtnm gngarmgncc ngtn gcnytn gargcngary tngcnytnac nytna argtn 360
 ytngargcng cngcnggncc ngcnytn gar gaygtnytn aycarcnytn ncayacnytn 420
 caycayathy tnwsncaryt ncargcntgy athcarccnc arccnacngc nggnccnmgn 480
 ccnmngggnm gnytnca yca ytggytnca y mgnytn c arg argcnccnaa raargarwsn 540
 gcnggntggy tngargcnws ngtnacntty aayytntty gnytnytnac nmnggayytn 600
 aartaygtng cngayggnga yytn tgyytn mgnacnwsna cncayccnga rwsnacntrr 660

<210> 11
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (17)...(628)

<400> 11
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 1 5 10
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 Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val Pro Thr Ser
 15 20 25
 aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa tct 148
 Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser
 30 35 40
 ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc ttg 196
 Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu
 45 50 55 60

gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc ttc	244
Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe	
65 70 75	
ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct gtg	292
Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val	
80 85 90	
gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc gct	340
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala	
95 100 105	
gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc ctg	388
Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu	
110 115 120	
cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc aca	436
His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr	
125 130 135 140	
gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg ctc	484
Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu	
145 150 155	
cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct gtc	532
Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val	
160 165 170	
acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg gcc	580
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala	
175 180 185	
gat ggg gac ctg tgt ctg aga acg tca acc cac cct gag tcc acc tga	628
Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr His Pro Glu Ser Thr *	
190 195 200	

<210> 12

<211> 203

<212> PRT

<213> Homo sapiens

<400> 12

Met Val Pro Thr Thr Leu Ala Trp Thr Val Val Leu Val Thr Leu Val	
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Leu Gly Leu Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr	
20 25 30	
Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln	
35 40 45	
Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu	
50 55 60	
Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp	
65 70 75 80	
Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala	
85 90 95	
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala	
100 105 110	
Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu	
115 120 125	
Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg	
130 135 140	
Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro	

145		150		155		160									
Lys	Lys	Glu	Ser	Ala	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu
				165					170					175	
Phe	Arg	Leu	Leu	Thr	Arg	Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asp	Leu
			180					185					190		
Cys	Leu	Arg	Thr	Ser	Thr	His	Pro	Glu	Ser	Thr					
		195					200								

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mgnttyaarw snytnwsncc ncargarytn gcnwsnttya araargcnmg ngaygcnytn	180
gargarwsny tnaarytnaa raaytggsn tgywsnwsnc cngtnttycc nggnaaytg	240
gayytnmgny tnytnargt nmngngarmgn ccngtnngcny tngargcnga rytngcnytn	300
acnytnaarg tnytnargc ngcngcnggn ccngcnytn argaygtnyt ngaycarccn	360
ytncaayacny tncaycayt hytnwsncar ytnargcnt gyathcarcc ncarccnacn	420
gcnggncnrm gncnmgngg nmgnytncay caytggytnc aymgnytnca rgargcnccn	480
aaraargarw sngcnggntg yytnargcn wsngtnacnt tyaayytntt ymgnytnytn	540
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[illegible]